
MASSRCH

(TM)

Release 2.1D John F. Collins, Blocomputing Research Unit.
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MPsrch_nnn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Jan 8 21:47:01 1998; MasPar time 1479.76 Seconds
Tabular output not generated. 1200.843 Million cell updates/sec

Title: >US-08-943-776-5
Description: (1-1251) from US08943776.seq
Perfect Score: 1251
N.A. Sequence: 1 GTGACATGAGGACGCGCT.....GTGGCCGCGTGTGGCGCGC 1251
Comp: CAGCTGTACTCCGCGCGCA.....CACCGGCGACTACGCGCGC

Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 430261 seqs, 710217276 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-new7
1: BCT 2: FUN 3: GEN 4: HTG1 5: HTG2 6: HTG3 7: HTG4 8: HDM1
9: HDM2 10: HDM3 11: INV1 12: INV2 13: ORG 14: MAM 15: VRT
16: PLN 17: PRO1 18: PRO2 19: ROD 20: SYN 21: UNC 22: VTR
genbank101
23: BCT1 24: BCT2 25: BCT3 26: BCT4 27: BCT5 28: BCT6 29: BCT7
30: BCT8 31: BCT9 32: BCT10 33: BCT11 34: BCT12 35: BCT13
36: GEN1 37: GEN2 38: GEN3 39: GEN4 40: GEN5 41: GEN6 42: HTG1
43: HTG2 44: HTG3 45: HTG4 46: HTG5 47: INV1 48: INV2 49: INV3
50: INV4 51: INV5 52: INV6 53: INV7 54: INV8 55: INV9 56: INV10
57: INV11 58: INV12 59: MAM1 60: MAM2 61: MAM3 62: VRT1
63: VRT2 64: VRT3 65: VRT4 66: PAT1 67: PAT2 68: PAT3 69: PAT4
70: PAT5 71: PAT6 72: PAT7 73: PHG 74: PLN1 75: PLN2 76: PLN3
77: PLN4 78: PLN5 79: PLN6 80: PLN7 81: PLN8 82: PLN9 83: PLN10
84: PLN11 85: PLN12 86: PR11 87: PR12 88: PR13 89: PR14
90: PR15 91: PR16 92: PR17 93: PR18 94: PR19 95: PR110
96: PR111 97: PR112 98: PR113 99: PR114 100: PR115 101: PR116
102: PR117 103: ROD1 104: ROD2 105: ROD3 106: ROD4 107: ROD5
108: ROD6 109: ROD7 110: ROD8 111: ROD9 112: STR 113: SYN
114: UNA
genbank101
115: VRL1 116: VRL2 117: VRL3 118: VRL4 119: VRL5 120: VRL6
121: VRL7 122: VRL8 123: VRL9 124: VRL10 125: VRL11
genbank-new7
126: BCT 127: GEN 128: HTG1 129: HTG2 130: INV 131: MAM
132: VRT 133: PHG 134: PLN1 135: PLN2 136: PR11 137: PR12
138: ROD 139: SYN 140: UNA 141: VRL
u-emb151_101
142: part1 143: part2

Statistics: Mean 11.267; Variance 5.572; scale 2.022
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	406	32.5	1198	96	HSU94504	Human lymphocyte asso	0.00e+00
2	392	31.3	1634	96	HSU74611	Human Apo-3 mRNA, com	1.32e-296
3	390	31.2	1254	96	HSU94501	Human lymphocyte asso	6.74e-295
4	390	31.2	1254	96	HSU72763	Human death receptor	6.74e-295
5	390	31.2	1254	96	HSU78029	Human apoptosis induci	6.74e-295
6	390	31.2	1557	95	HSU73380	Human apoptosis-media	6.74e-295
7	388	31.0	1528	95	HSU83597	Human death domain re	3.44e-293
8	374	29.9	1257	96	HSU94502	Human lymphocyte asso	3.04e-281
9	360	28.8	1119	96	HSU94509	Human lymphocyte asso	2.60e-269
10	341	27.3	1355	96	HSU94503	Human lymphocyte asso	3.87e-253
11	339	27.1	1743	96	HSU94511	H sapiens mRNA for WS	1.94e-251
12	317	25.3	705	96	HSU94508	Human lymphocyte asso	9.38e-233
13	317	25.3	952	96	HSU94506	Human lymphocyte asso	9.38e-233
14	317	25.3	1087	96	HSU94505	Human lymphocyte asso	9.38e-233
15	317	25.3	1143	96	HSU94510	Human lymphocyte asso	9.38e-233
16	300	24.0	838	96	HSU94507	Human lymphocyte asso	2.40e-218
17	177	14.1	808	95	HSU75381	Human apoptosis-media	2.55e-115
18	177	14.1	809	96	HSU94512	Human lymphocyte asso	2.55e-115
19	177	14.1	816	95	HSU83598	Human death domain re	2.55e-115
20	171	13.7	651	95	HSU83599	Human alternatively s	2.24e-110
21	80	6.4	665	95	HSU83600	Human death domain re	1.27e-37
22	53	4.2	281	96	HSU94511	Human lymphocyte asso	8.99e-13
23	40	3.2	215	71	I28278	Sequence 5 from paten	5.5e-03
24	37	3.0	1803	54	DROPHRFRN2	Drosophila virilis FM	4.50e-03
25	35	2.8	2431	111	RNU61184	Rattus norvegicus ary	7.92e-04
26	35	2.8	4180	111	RNU49058	Rattus norvegicus CTD	7.92e-04
27	34	2.7	215	71	I28278	Sequence 5 from paten	3.38e-03
28	34	2.7	216	98	HUMHUNTEPA	Homo sapiens huntingt	3.38e-03
29	34	2.7	614	98	HUMHUN01	Homo sapiens huntingt	3.38e-03
30	34	2.7	3326	52	DRAC000890	Drosophila melanogast	3.38e-03
31	34	2.7	4105	98	HUMHDLA	Homo sapiens (clone)	3.38e-03
32	34	2.7	10348	98	HUMHDLA	Homo sapiens huntingt	3.38e-03
33	34	2.7	40592	92	HSU191F1	Equus caballus TATA-b	1.27e-04
34	33	2.6	190	60	HRSTBPRA	H sapiens transcripti	1.27e-04
35	33	2.6	920	93	HSTFIIDAA	Human transcription f	1.27e-04
36	33	2.6	1035	101	HUMFIID	Human TATA-binding pr	1.27e-04
37	33	2.6	1876	101	HUMFIID	Sus scrofa p55 TMR re	1.27e-04
38	33	2.6	2004	61	SSU19994	Rat tumor necrosis fa	1.27e-04
39	33	2.6	2130	110	RATTNFR	Drosophila melanogast	1.27e-04
40	33	2.6	2742	53	DMU82273	Pinctada fucata mRNA	1.27e-04
41	33	2.6	3331	12	PRD074	Drosophila virilis ma	1.27e-04
42	33	2.6	5650	54	DROMASTM	Human Notch4 (hNotch4	1.27e-04
43	33	2.6	6122	96	HSU95299	Human DNA for NOTCH4	1.27e-04
44	33	2.6	19654	9	HSD566	Human DNA for NOTCH4	1.27e-04
45	33	2.6	19654	86	D86566	Human DNA for NOTCH4	1.27e-04

ALIGNMENTS

RESULT 1
LOCUS HSU94504 1198 bp mRNA PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 3 mRNA, alternatively spliced, complete cds.
ACCESSION U94504
NID 92071954
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1198)
AUTHORS Sreaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R., McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing

2
 RESULT HSU74611 1634 bp mRNA
 LOCUS Human Apo-3 mRNA, complete cds.
 DEFINITION U74611
 ACCESSION g1763292
 NID
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrates; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 1634)
 Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pitti,R.M., Gray,C.L.,
 Goddard,A.D., Bauer,K.D. and Ashkenazi,A.
 Apo-3, a new member of the tumor necrosis factor receptor family,
 contains a death domain and activates apoptosis and NF-kB
 Curr. Biol. (1996) ~~5~~ 1669-1676
 2 (bases 1 to 1634)
 Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pitti,R.M., Gray,C.L.,
 Goddard,A.D., Bauer,K.D. and Ashkenazi,A.
 Direct Submission
 Submitted (15-OCT-1996) Molecular Oncology, Genentech, 460 Pt. San
 Bruno Blvd., South San Francisco, CA 94080, USA
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Matches					
Conservative					
Mismatches					
Indels					
Gaps					
Score					
Pred. No.					
Length					

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Db	102	ctgtgccggfagctctccacaagaagattggctgttttggttgacagagctccacagcggg	161
QY	123	CTGTGCCACTGAGTCCCAAGAAAGGATATGGCCGCTTTTGTGTGAGGGGCTGCCAAGGG	182
Db	162	gcactacctgaaggcccttgcacgagacctcggcgcaactccactcctctgtgtgtcc	221
QY	183	ACACTACATGAAAGGCCCTGCGCAGAACCTGTGGCAACTCCACCTGCTCCCTGTCC	242
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QY	243	CTCGGACACCTTCTTGACCAGAGAACACACTTTAAGACTGACTATCCGCTGCCAAGT	302
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QY	363	CTGTGCTGCCAGTCAGGCTGTGTGTGACTGCTCCACCAGGCCATGTGGGAAAGCTC	422
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QY	423	ACCTTCTCTTGNT-C---CC---A-TGCGGGG--TACAAC---AC-CA--G-T-C-	462
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QY	463	CA--T--G-AG-GCTCCAACCCCGGCCCTGCCTGCTGCTCTATATACGTGGGCAA	515
Db	522	tgctcgtgtcctgcccaacagacacctggggagctgtccagagcgtgtgcgcgtgt	581
QY	516	TGACTGCAGCTCTGCCCCACAGGGCTTGACAGAGCGTTGCCCTTAAGGCTTGACACTGC	575
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QY	576	CTGTGGCTGGAACAGATGTTTGGGTCCAGGTGCT--T--CTAG---GAG-TGCGGTT	626
Db	642	cctgcttggggccacccctgacctacacataacgcgcaactgtgacctcacaagccctggt	701
QY	627	CCTTTTGGGGCTATCCTGATCTGCATATTGTGATGGACGCTTGTAAAGCCGCTGT	686
Db	702	tactcgagatgaagctggatgagccttgacccacacacggccacccatctgtcacc	761
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Db	820	-gtccagttgggttaacagctggacccttgctaccccgagacccagagagcgctctg	878
QY	807	TGTCCAGTTGGTAGGCAACAACCTGGACCCCTGGCTTATCCGACTCTCAGGAGTGGTCTG	866
Db	879	cccgacagtgacatggtcctcgtgacacagttgcccagcagagctcttggcccgcgtgctc	938
QY	867	CGGACAGGCTCAACACCCCTGGGATCAGCTGCCAAACAGAACTCTTTGGAACTCCTCTGCG	926
Db	938	gggacacactctccacagatccgacagcgactcgcgagcccatatctctcagcggcgccc	998

QY	927	ATCTCCGCTCTCGCCAGCGCCCCCTCGGGGCTCTCCGGCTGCTGTGCTCCAGGCTGGCCC	989
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QY	987	GCAGCTCTACGATGTGATGGATCGGGTCCCAGCAGCAAGGTGGAAAGAGTTCGTGCGCAC	1046
Db	1059	gctggggctgcgcgaggcagagatcgaaagccgtggaggtggagatcgccgcttccagag	1118
QY	1047	GCTGGGGCTCGCGGAAGCGGAAATTGAAGCCGTCGGAGTGGAAATCTGCCGCTTCCGAGA	1107
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QY	1107	CCAGCAGTATGAGATGCTCAAGCGCTGCGGTCCAGCAGCAGCCTGCAGGCTCTGGTGGCAI	1166
Db	1179	ttacgcggccctggagcgcattgggctggaacggtcgtggaagacitcggcagccgcct	1239
QY	1167	CTATGGGGCTCTGGAGCGCATGGGTCTGGAAGGCTGTGCCAGGACCTGCCAGACCGGCT	1226
Db	1239	gcagcgcggcccgtaga	1254
QY	1227	GCAGCTGGCCCGTGA	1242

RESULT	4	HSU72763	1254 bp	mRNA	PRI	15-NOV-1996
LOCUS		Human death receptor 3 (DR3)	mrna, complete cds.			
DEFINITION		U72763				
ACCESSION		g1669511				
NID						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
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TITLE						
JOURNAL						
FEATURES						

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ORIGIN		

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Best Local Similarity 74.7%; Pred. No. 6.74e-295;
Matches 908. Conservative 0; Mismatches 266; Indels 42

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Dbb 102 ctgtgcccgttgacttcacaaagaatggctgttgtttgtgcagaggctgccagcggg 161

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Dbb 162 gaactacctgaaggcccttgcaaggagccctgcggcaactcgcccaactccactgcttgtgtcc 221

QY 183 ACACATACATGAAGGCCCTCGGCAGAACCCTGTGGCAACTCCACCTGCCCTCCCTGCTCC 242

Dbb 222 ccaagacaccctcttggtgctggggaacacacataattctgaattgccccgctgcccaggc 281

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QY	1167	CTATCGCGCTCTGGAGCGCATGGGTCTGTGAAGGCTGTGCCGAGGACTCTCGCAGCGGCT	1226
Db	1239	gcagcgcggcccgctga	1254
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ACCESSION	U78029		complete cds.
NID	g1778763		
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;		
	Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (bases 1 to 1254)		
AUTHORS	Degli-Esposti,M.A., Din,W.S., Cosman,D., Smith,C.A. and Goodwin,R.G.		
TITLE	AIR, A Novel Member of the TNF Receptor Family, Is a Strong Inducer of Apoptosis		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1254)		
AUTHORS	Degli-Esposti,M.A. and Goodwin,R.G.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51 University St., Seattle, WA 98101, USA		
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QY	183	ACACTACATGAAGCCCCCTGCGCAGAACCTGTGGCAACTCCACCTGCCCTTCCCTGTCC	242
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